

## SEQUENCE LISTING

<110> Holloway, James L.  
Lok, Si

<120> SECRETED PROTEIN · ZACRP4

<130> 99-29

<150> 60/141.928  
<151> 1999-07-01

<160> 9

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1357

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (210)...(1196)

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 ggagcccccg ccgccccctgc cgcaagcgcg gcggtcagcg cgcaagccggg caccgcagc 120  
 ctgcagcctg cagcccgcag cccgcagccc ggagccagat cgccggctca gaccgaaccc 180  
 gactcgaccg ccgccccccag ccaggcgcc atg ctg ccg ctt ctg ctg ggc ctg 233  
 Met Leu Pro Leu Leu Leu Gly Leu  
 1 5

ctg ggc cca gcg gcc tgc tgg gcc ctg ggc ccg acc ccc ggc ccg gga 281  
Leu Gly Pro Ala Ala Cys Trp Ala Leu Gly Pro Thr Pro Gly Pro Gly  
10 15 20

tcc tct gag ctg cgc tcg gcc ttc tcg gcg gca cgc acc acc ccc ctg 329  
Ser Ser Glu Leu Arg Ser Ala Phe Ser Ala Ala Arg Thr Thr Pro Leu  
25 30 35 40

gag ggc acg tcg gag atg gcg gtg acc ttc gac aag gtg tac gtg aac 377  
Glu Gly Thr Ser Glu Met Ala Val Thr Phe Asp Lys Val Tyr Val Asn

45	50	55	
atc ggg ggc gac ttc gat gtg gcc acc ggc cag ttt cgc tgc cgc gtg Ile Gly Gly Asp Phe Asp Val Ala Thr Gly Gln Phe Arg Cys Arg Val			425
60	65	70	
ccc ggc gcc tac ttc ttc tcc acg gct ggc aag gcc ccg cac aag Pro Gly Ala Tyr Phe Phe Ser Phe Thr Ala Gly Lys Ala Pro His Lys			473
75	80	85	
agc ctg tcg gtg atg ctg gtg cga aac cgc gac gag gtg cag gcg ctg Ser Leu Ser Val Met Leu Val Arg Asn Arg Asp Glu Val Gln Ala Leu			521
90	95	100	
gcc ttc gac gag cag cg <sup>g</sup> cgg cca ggc gcg cg <sup>g</sup> cgc gca gcc agc cag Ala Phe Asp Glu Gln Arg Arg Pro Gly Ala Arg Arg Ala Ala Ser Gln			569
105	110	115	120
agc gcc atg ctg cag ctc gac tac ggc gac aca gtg tgg ctg cgg ctg Ser Ala Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg Leu			617
125	130	135	
cat ggc gcc ccg cac tac gc <sup>g</sup> cta ggc gc <sup>g</sup> ccc ggc gcc acc ttc agc His Gly Ala Pro His Tyr Ala Leu Gly Ala Pro Gly Ala Thr Phe Ser			665
140	145	150	
ggc tac cta gtc tac gcc gac gcc gac gct gac gc <sup>g</sup> cct gc <sup>g</sup> cgc ggg Gly Tyr Leu Val Tyr Ala Asp Ala Asp Ala Asp Ala Pro Ala Arg Gly			713
155	160	165	
ccg ccc gc <sup>g</sup> ccc ccc gag ccg cgc tcg gcc ttc tcg gc <sup>g</sup> gc <sup>g</sup> cgc acg Pro Pro Ala Pro Pro Glu Pro Arg Ser Ala Phe Ser Ala Ala Arg Thr			761
170	175	180	
cg <sup>c</sup> agc ttg gtg ggc tcg gac gct ggc ccc ggg ccg cgg cac caa cca Arg Ser Leu Val Gly Ser Asp Ala Gly Pro Gly Pro Arg His Gln Pro			809
185	190	195	200
ctc gcc ttc gac acc gag ttc gtc aac att ggc ggc gac ttc gac gc <sup>g</sup> Leu Ala Phe Asp Thr Glu Phe Val Asn Ile Gly Gly Asp Phe Asp Ala			857
205	210	215	
g <sup>c</sup> gc <sup>g</sup> ggc gtg ttc cgc tgc cgt ctg ccc ggc gcc tac ttc ttc tcc Ala Ala Gly Val Phe Arg Cys Arg Leu Pro Gly Ala Tyr Phe Phe Ser			905
220	225	230	

ttc acg ctg ggc aag ctg ccg cgt aag acg ctg tcg gtt aag ctg atg 953  
 Phe Thr Leu Gly Lys Leu Pro Arg Lys Thr Leu Ser Val Lys Leu Met  
   235                         240                         245  
  
 aag aac cgc gac gag gtg cag gcc atg att tac gac gac ggc gcg tcg 1001  
 Lys Asn Arg Asp Glu Val Gln Ala Met Ile Tyr Asp Asp Gly Ala Ser  
   250                         255                         260  
  
 cg~~g~~ cgc cgc gag atg cag agc cag agc gtg atg ctg gcc ctg cgg cgc 1049  
 Arg Arg Arg Glu Met Gln Ser Gln Ser Val Met Leu Ala Leu Arg Arg  
   265                         270                         275                         280  
  
 ggc gac gcc gtc tgg ctg ctc agc cac gac cac gac ggc tac ggc gcc 1097  
 Gly Asp Ala Val Trp Leu Leu Ser His Asp His Asp Gly Tyr Gly Ala  
   285                         290                         295  
  
 tac agc aac cac ggc aag tac atc acc ttc tcc ggc ttc ctg gtg tac 1145  
 Tyr Ser Asn His Gly Lys Tyr Ile Thr Phe Ser Gly Phe Leu Val Tyr  
   300                         305                         310  
  
 ccc gac ctc gcc ccc gcc gcc ccg ccg ggc ctc ggg ggc tcg gag cta 1193  
 Pro Asp Leu Ala Pro Ala Ala Pro Pro Gly Leu Gly Ala Ser Glu Leu  
   315                         320                         325  
  
 ctg tgagccccgg gccagagaag agcccggag ggccaggggc gtgcatgcca 1246  
 Leu  
  
 ggccggggcc gaggctgaa agtcccgcbc gagcgccacg gcctccggc ggcgcctggac 1306  
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 Leu Gly Pro Thr Pro Gly Pro Gly Ser Ser Glu Leu Arg Ser Ala Phe  
   20                 25                 30  
 Ser Ala Ala Arg Thr Thr Pro Leu Glu Gly Thr Ser Glu Met Ala Val  
   35                 40                 45  
 Thr Phe Asp Lys Val Tyr Val Asn Ile Gly Gly Asp Phe Asp Val Ala  
   50                 55                 60

Thr Gly Gln Phe Arg Cys Arg Val Pro Gly Ala Tyr Phe Phe Ser Phe  
 65 70 75 80  
 Thr Ala Gly Lys Ala Pro His Lys Ser Leu Ser Val Met Leu Val Arg  
 85 90 95  
 Asn Arg Asp Glu Val Gln Ala Leu Ala Phe Asp Glu Gln Arg Arg Pro  
 100 105 110  
 Gly Ala Arg Arg Ala Ala Ser Gln Ser Ala Met Leu Gln Leu Asp Tyr  
 115 120 125  
 Gly Asp Thr Val Trp Leu Arg Leu His Gly Ala Pro His Tyr Ala Leu  
 130 135 140  
 Gly Ala Pro Gly Ala Thr Phe Ser Gly Tyr Leu Val Tyr Ala Asp Ala  
 145 150 155 160  
 Asp Ala Asp Ala Pro Ala Arg Gly Pro Pro Ala Pro Pro Glu Pro Arg  
 165 170 175  
 Ser Ala Phe Ser Ala Ala Arg Thr Arg Ser Leu Val Gly Ser Asp Ala  
 180 185 190  
 Gly Pro Gly Pro Arg His Gln Pro Leu Ala Phe Asp Thr Glu Phe Val  
 195 200 205  
 Asn Ile Gly Gly Asp Phe Asp Ala Ala Gly Val Phe Arg Cys Arg  
 210 215 220  
 Leu Pro Gly Ala Tyr Phe Ser Phe Thr Leu Gly Lys Leu Pro Arg  
 225 230 235 240  
 Lys Thr Leu Ser Val Lys Leu Met Lys Asn Arg Asp Glu Val Gln Ala  
 245 250 255  
 Met Ile Tyr Asp Asp Gly Ala Ser Arg Arg Arg Glu Met Gln Ser Gln  
 260 265 270  
 Ser Val Met Leu Ala Leu Arg Arg Gly Asp Ala Val Trp Leu Leu Ser  
 275 280 285  
 His Asp His Asp Gly Tyr Gly Ala Tyr Ser Asn His Gly Lys Tyr Ile  
 290 295 300  
 Thr Phe Ser Gly Phe Leu Val Tyr Pro Asp Leu Ala Pro Ala Ala Pro  
 305 310 315 320  
 Pro Gly Leu Gly Ala Ser Glu Leu Leu  
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<211> 31

<212> PRT

<213> Artificial Sequence

<220>

<223> C1q Aromatic Motif

<221> VARIANT

<222> (2)...(6)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (7)...(7)

<223> Xaa is asparagine or aspartic acid

<221> VARIANT

<222> (8)...(11)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (12)...(12)

<223> Xaa is phenylalanine, tyrosine, tryptophan or  
leucine

<221> VARIANT

<222> (13)...(18)

<223> Each Xaa is independently any amino acid residue

<221> VARIANT

<222> (20)...(24)

<223> Each Xaa is independently any amino acid residue

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<222> (26)...(26)

<223> Xaa is any amino acid residue

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<222> (28)...(28)

<223> Xaa is any amino acid residue

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<222> (30)...(30)

<223> Xaa is any amino acid residue

<221> VARIANT

<222> (31)...(31)

<223> Xaa is phenylalanine or tyrosine

<400> 3

Phe Xaa Xaa

1

5

10

15

Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Gly Xaa Tyr Xaa Phe Xaa Xaa

20

25

30

<210> 4  
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 <212> DNA  
 <213> Artificial Sequence

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 <223> Degenerate nucleotide sequence encoding the polypeptide of SEQ ID NO:2

<221> variation  
 <222> (1)...(987)  
 <223> Each N is A, T, G or C

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atgytnccny tnytnytnnn	60
ccngcngcnt gytggcnyt ngnccnacn	120
ccnggncng gnwsnwsnga rytnmgnwsn gcnttywsng cngcmgnac nacnccnytn	180
garggnacnw sngaratggc ntgnacntty gayaargtnt aygttaayat hggngngay	240
ttygaygtng cnacnggnca rttymgntgy mnngtnccng gngctaytt yttywsntty	300
acngcngna argnccnca yaarwsnytn wsngtnatgy tngtnmgnna ymgngaygar	360
gtncargcny tngcnttyga ygarcarmgn mnngcnngng cnmgnmgnnc ncwnwsncar	420
wsngcnatgy tncarytna ytayggngay acngtntggy tnmgnytnca yggngcnccn	480
caytaygcny tngngcncc nnngcnacl ttywsngnt ayytngtna ygcngaygc	540
gaygcngayg cnccngcnmg nnngccnccn gcncnccng arccmgnws ncnttywsn	600
gnngcnmgna cnmgnwsnyt ntnggnwsn gaygcngngc nnngccnmg ncaycarccn	660
ytngcnttyg ayaengartt ygttaayath ggngngayt tygagcngc ncngngn	720
ttymgntgy gnytnccnng ncntayttty wsnttya cnytngnna rytnccnmgn	780
aaracnytnw sngtnaaryt natgaaraay mnngaygarg tncargcnat gathtaygay	840
gayggngcnw smgnmgnrmg ngaratgcar wsncarwsng tnatgytngc nytnmgnmgn	900
ggngaygcng ntnggytnyt nwsncaygay caygayggnt ayggngccta ywsnaaycay	960
gnnaartaya thacnttyws ngnntyytn gtntayccng ayytngcncc ncngcnccn	
ccnggnytn gngcnwsnga rytnytn	987

<210> 5  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide ZC20,839

<400> 5  
 atgtacttgc cgtggttgct gtag

<210> 6

200516202205

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC20840

<400> 6

cgacaccgag ttcgtcaaca ttg

23

<210> 7

<211> 325

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate nucleotide sequence encoding the polypeptide of SEQ ID NO:2.

<221> variation

<222> (1)...(325)

<223> Each N is independently A, T, C or G.

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gcgacttcga cgccgcggcc ggcgttcc gctccgtct gnccggcgcc tacttcttct	120
ncttcacgct gggcaagctg ccgcgttaaga cgctgtcggt taagctgatg aagaaccgcg	180
acgagggtgca ggcatgatt tacgacgacg gcgcgtcgcg gcgcgcgag atgcagagcc	240
agagcgtgat gctggccctg cggcgccgng acgcccgtctg gctgtcagcc acgaccacga	300
cggctacggc gcctacagca accac	325

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide ZC22162

<400> 8

ccgcggcacca aaccactc

18

<210> 9

<211> 18

<212> DNA  
<213> Artificial Sequence

<220>  
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gtcgcggttc ttcatcag

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:: . :  
Clq 2 FDTEFVNIGGDFDAAAGVFRCRLPGAYFFSFTLGKLPRKTLVKLMKNRDEVQAMIYDDG

Clq 1 RRPGARRAASQSAMLQLDYGDTVWL  
: . : : : : : : : :  
Clq 2 ASR-RREMQSQSVMLALRRGDAVWL

**Figure**